

Alpha Viruses nsp2 alignment

CLUSTAL W (1.82) multiple sequence alignment

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SFV_nsp2      GVVETPRSALKVTAQPNDVLLGNVVLSPQTVLKSSKLAPVHPLAEQVKIITHNGRAGGY 60
RRV_nsp2      GVVETPRNALKVTPQERDQLIGAYLILSPQTVLKSEKLTPIHPLAEQVTIMTHSGRSGRY 60
ONV_nsp2      GIVETPRGAIKVTAQPSDLVVGEYLVLTPOAVLRSQKLSLIHALAEQVKTCTHSGRAGRY 60
SinV_nsp2     ALVETPRGHVRIIPQANDRMIGQYIVVSPNSVLKNAKLAPAHPLADQVKIITHSGRSGRY 60
VEEV_nsp2     GSVETPRGLIKVTSYAGEDKIGSYAVLSPQAVLKSEKLSCHPLAEQVIVITHSGRKGRY 60
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SFV_nsp2      QVDGYDGRVLLPCGSAIPVPEFQALSESATMVYNREFVNRKLYHIAVHGPSLNTDEENY 120
RRV_nsp2      PVDRYDGRVLPVTGAAIPVSEFQALSESATMVYNREFINRKLHHIALYGPALNTDEENY 120
ONV_nsp2      AVEAYDGRVLPVSGYAIPOEDFQSLSESATMVFNREFVNRKLHHIAMHGPAALNTDEESY 120
SinV_nsp2     AVEPYDAKVLMPAGGAVPWPEFLALSESATLVYNREFVNRKLYHIAMHGPAKNTDEEQY 120
VEEV_nsp2     AVEPYHGKVVVPEGHAIPVQDFQALSESATIVYNREFVNRKLYHIAHGHGALNTDEEY 120
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SFV_nsp2      EKVRAERTDAEYVFDVDDKKCCVKREEASGLVLVGELTNPPFHEFAYEGLKIRPSAPYKTT 180
RRV_nsp2      EKVRAERAEEYVFDVDDKRTCKVKREDASGLVLVGDLINPPFHEFAYEGLKIRPATPFQTT 180
ONV_nsp2      ELVRVEKTEHEYVYVDVQKKCKREEATGLVLVGDLTSPPYHEFAYEGLKIRPACPYKTA 180
SinV_nsp2     KVTKAELAETHEYVFDVDDKKRCVKKEEASGLVLSGELTNPPYHELALEGLKTRPAVPYKVE 180
VEEV_nsp2     KTVKPSEHDGEYLYIDRQKQCVKKELVTLGLTGLVDPFHEFAYESLRTPAAPYQVP 180
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SFV_nsp2      VVGVGVPVPGSGKSIIKSLVTKHDLVTSKKKENCQEIVNDVKKHRGKTSRENSDSILLN 240
RRV_nsp2      VIGVGVPVPGSGKSIIKSVVTTTRDLVASGKKENCQEIVNDVKKQRLDVTARTVDSILLN 240
ONV_nsp2      VIGVGVPVPGSGKSIIKNLVTRQDLVTSKKKENCQEISNDVMRQKLEISARTVDSILLN 240
SinV_nsp2     TIGVIGTPGSGKSIIKSTVTARDLVTSKKKENCRIEADVLRRLRGMQITSKTVDVSMNL 240
VEEV_nsp2     TIGVYGVPGSGSGSIKSAVTKKDLVSAKKENCAEIIIRDVKKMKGLDVNARTVDSVLLN 240
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SFV_nsp2      GCRRAVDILYVDEAFACHSGTLLALIALVKPRSKVVLCDPKQCGFFNMQLKVNFNH-- 298
RRV_nsp2      GCRRGVENLYVDEAFACHSGTLLALIAMVKPTGKVLCDPKQCGFFNLMQLKVNFNH-- 298
ONV_nsp2      GCNKPVLEVLYVDEAFACHSGTLLALIAMVRPRQKVVLCGDPKQCGFFNMQMKNVYNH-- 298
SinV_nsp2     GCHKAVEVLYVDEAFACHAGALLALIAIVRPRKKVVLCDPDMQCGFFNMQLKVNHNPE 300
VEEV_nsp2     GCKHPVETLYIDEAFACHAGTLRALIAIRPK-KAVLCGDPKQCGFFNMCLKVHFNH-- 297
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SFV_nsp2      -NICTEVCHKSISRRCRTPVTAIVSTLHYGKMRTTNPCNKPIIIDTTGQTKPKPGDIVL 357
RRV_nsp2      -DICTQVLHKSISRRLTPITAIVSTLHYQGKMRTTNLCSAPIQIDTTGTTKPAKGDIVL 357
ONV_nsp2      -NICTQVYHKSISRRLTPVTAIVSSLHYESKMRTTNQPIVVDTTGITKPEPGDLVL 357
SinV_nsp2     KDICTKTFYKISRRCRTPVTAIVSTLHYDGKMRTTNPCCKNIEIDITGATKPKPGDIIL 360
VEEV_nsp2     -EICTQVFHKSISRRCRTPVTSVSTLFYDKRMRTTNPKETKIVIDTTGSTKPKQDDLIL 356
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SFV_nsp2      TCFRGWAKQLQLDYRGHEVMTAAASQGLTRKGVYAVRQKVNENPLYAPASEHVNVLTRT 417
RRV_nsp2      TCF--WVKQLQIDYRGHEVMTAAASQGLTRKGVYAVRQKVNENPLYAPSEHVNVLTRT 415
ONV_nsp2      TCFRGWVKQLQIDYRGNEVMTAAASQGLTRKGVYAVRQKVNENPLYAPTSEHVNVLTRT 417
SinV_nsp2     TCFRGWVKQLQIDYRGHEVMTAAASQGLTRKGVYAVRQKVNENPLYAITSEHVNVLTRT 420
VEEV_nsp2     TCFRGWVKQLQIDYKGNEMTAAASQGLTRKGVYAVRYKVNENPLYAPTSEHVNVLTRT 416
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SFV_nsp2      EDRLVWKTLAGDPWIKVLSNIPQGNFTATLEEWQEEHDKIMKVIEGPAAPVDAFQNKANV 477
RRV_nsp2      ENRLVWKTLSGDPWIKVLTNIPKGFDSATLEEWQEEHKNIMNALRERSTAVDPFQNKAKV 475
ONV_nsp2      EGKLTWKTLSGDPWIKILQNPPKGFATIKWEAEHASIMAGICNHQMAFDVFNKANV 477
SinV_nsp2     EDRLVWKTLSGDPWIKOPTNIPKGNFQATIEDWEAEHKGIIAAINSPTPRANPFSCKTNV 480
VEEV_nsp2     EDRLVWKTLAGDPWIKILTAKYPGNFTATIEEWQAEHDAIMRHILERPDPTDVFQNKANV 476
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SFV_nsp2      CWAKSLVPVLDTAGIRLTAAEWSTIITAFKEDRAYSPVVALNEICTKYYGVLDLSDGLFSA 537
RRV_nsp2      CWAKCLVQVLETAGIRMTAAEWDTVL-AFREDRAYSPEVALNEICTKYYGVLDLSDGLFSA 534
ONV_nsp2      CWAKCLVPILDTAGIKLSDRQWSQIVQAFKEDRAYSPEVALNEICTRIYGVLDLSDGLFSK 537
SinV_nsp2     CWAKALEPILATAGIVLTGCQWSELFPQFADDKPHSAIYALDVICIKFFGMDLTSGLFSK 540
VEEV_nsp2     CWAKALVPVLKTAGIDMTTEQWNTVD-YFETDKAHSAEIVLNQLCVRFFGLDLSGLFSA 535
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SFV_nsp2	PKVSLYYENN-----HWDNRPGGRMYGFNAATAARLEARHTFLKGQWHTGKQAVIAER	590
RRV_nsp2	QSVSLYYENN-----HWDNRPGGRMYGFNREVARKFEQRYPFRLGKMDSGLQVNVPER	587
ONV_nsp2	PLISVYYADN-----HWDNRPGGKMFGFNPEVALMLEKKYPFTKGKWNINKQICITTR	590
SinV_nsp2	QSIPLTYHPADSARPVAHWDNSPGTRKYGYDHAIAAELSRFPVFQ-LAGKGTQLDLQTG	599
VEEV_nsp2	PTVPLSIRNN-----HWDNSPSPNMYGLNKEVVRLSRRYPQLPRAVATGRVYDMNTG	588
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SFV_nsp2	KIQPLSVLDNVIPINRRRLPHALVAEYKTVKGSRVLEWLVNKVRGYHVLLVSEYNLALPRRR	650
RRV_nsp2	KVQPFNAECNILLNRRRLPHALVTSYQQCRGERVEWLLKKLPGYHLLLSEYNLALPHKR	647
ONV_nsp2	KVDEFNPETNII PANRRRLPHSLVAEHHSVRGERMEWLVNKISGHHMLLVSGHNLIPTKR	650
SinV_nsp2	RTRVISAQHNLVPVNRRLPHALVPEYKEKQPGPVKKFLNQFKHHSVLVVSEEKIEAPRKR	659
VEEV_nsp2	TLRNYDPRINLVPVNRRLPHALVLHNEHPQSDFSFVSKLKGRTVLVVG-EKLSVPGKK	647
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SFV_nsp2	VTWLSPLNVTGADRCYDLSLGLPADAGRFDLVFVNIHTEFRIHHYQQCVDHAMKLQMLGG	710
RRV_nsp2	VFWIAPPHVSGADRIYDLDLGLPLNAGRYDLVFVNIHTEYRTHHYQQCVDHSMKLQMLGG	707
ONV_nsp2	VTWVAPLGTGRADYTYNLELGLPATLGRYDLVVINIHTPFRHHYQQCVDHAMKLQMLGG	710
SinV_nsp2	IEWIAPIGIAGADKNYNLAFGFPQA-RYDLVFINIGTKYRNHHFQQCEDHAATLKTLSR	718
VEEV_nsp2	VDWLS--DQPEATFRARLDLGI PGDVPKYDIVFINVRTPYKYHHYQQCEDHAIKLSMLTK	705
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SFV_nsp2	DALRLLKPGG-ILMAYGYADKISEAVVSSLSRKFS SARVLRPDCVTSNTEVFLLFSNFD	769
RRV_nsp2	DSLHLL-PGGSLLIRAYGYADRVSEMVVTALARKFSAFRVLRPACVTSNTEVFLLFTNFD	766
ONV_nsp2	DSLRLKPGGSLLIRAYGYADRTSERVISVLGRKFRSSRALKPQCITSNTEMFLLFSRFD	770
SinV_nsp2	SALNCLNPGGTLVVKSYGYADRNSEDVVTALARKFVRVSAARPCVSSNTEMYLIFRQLD	778
VEEV_nsp2	KACLHLNPGGTCVSI GYGADRASESIIGAIARQFKFSRVCKPKSSHEETEVLVFEIGYD	765
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SFV_nsp2	NGK-RPSTLHQMNTKLSAVYAGEAMHTAGC	798
RRV_nsp2	NGR-RAVTLHQANQRLSSMFACNGLHTAGC	795
ONV_nsp2	NGR-RNFTTHVMNNQLNAVYAGLATR-AGC	798
SinV_nsp2	NSRTRQFTPHHLNCSVISVYEGTRDGVGA-	807
VEEV_nsp2	RKA-RTHNPYKLSSTLTNIYTGSRLHEAGC	794
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